Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1. (Currently amended) A method for the development of gene panels for diagnostic and therapeutic purposes, comprising the steps of:

a) isolating at least one biological sample from each of at least two groups of biological material containing mRNA and/or proteins~~, wherein each of said groups is cancerous~~;

b) analysing the expression level of at least one gene in at least one of the biological samples;

c) selecting the gene(s) exhibiting a different expression level between said at least two groups of biological material, whereby a first knowledge base is generated;

d) analysing the level of cytosine methylation of at least one gene of said first knowledge base in at least one of the biological samples of step a) by means comprising treatment with bisulphite, hydrogen sulphite or disulphite;

e) selecting gene(s) exhibiting a different level of cytosine methylation between said at least two groups of biological material, whereby a second knowledge base is generated;

f) adding selected genes from the second knowledge base to a gene panel; ~~and~~

g) repeating steps a) through f) at least five times; and

h) outputting the result in a user readable format.

2. (Previously presented) The method according to claim 1, comprising that the biological material is isolated by means of a biopsy, by means of an operation on an individual, by means of a dissection, derived from a preserved biological sample, collected from body fluid(s) and/or collected directly from the environment.

3. (Previously presented) The method according to claim 2, characterised in that the biological material comprises a eucaryotic and/or procaryotic cell line, a biopsy sample, blood, sputum, faeces, urine, cerebral liquid, tissue embedded in paraffin, tissue derived from eyes, intestine, brain, heart, prostata, kidney, lung, breast or liver, histological samples or a combination thereof.

4. (Previously presented) The method according to claim 1, characterised in that at least one of the biological samples is derived from biological material of diseased individuals.

5. (Previously presented) The method according to claim 1, characterised in that the isolation of said biological sample comprises isolating subcellular compartments, organelles, macromolecular structures and multiprotein complexes, partial or complete preparation of the mRNA, reverse transcription or partial digestion of the material with an enzyme selected from proteases, RNAses and/or DNAses or combinations thereof.

6. (Previously presented) The method according to claim 1, characterised in that the

analysis of the expression level of the at least one gene in the biological sample comprises determining the relative amount of mRNA or protein derived from said at least one gene.

7. (Previously presented) The method according to claim 6, characterised in that the analysis comprises one- or two-dimensional gel electrophoresis, differential display, analysis of selected sets of tumour markers, subtractive hybridisation, mass spectrometry, comparative expressed sequence tag sequencing, representational difference analysis, cDNA or oligonucleotide arrays, serial analysis of gene expression, enzymatic, fluorescent, radioactive, dye and/or antibody labelling.

8. (Previously presented) The method according to claim 7, characterised in that the analysis further comprises measuring intensities of expression during one- or two-dimensional gel electrophoresis, differential display, subtractive hybridisation, DNA, RNA or protein sequencing, mass spectrometry, and enzymatic, radioactive, dye and/or antibody labelling.

9. (Previously presented) The method according to claim 6, characterised in that the analysis is at least partially performed by means of at least one of a robot and a computer device.

10. (Previously presented) The method according to claim 6, characterised in that the expression levels of at least two genes are analysed in parallel.

11. (Previously presented) The method according claim 10, characterised in that the expression levels of at least 100 genes are analysed in parallel.

12. (Previously presented) The method according to claim 1, characterised in that the selection is based on a combination of the analysis of both mRNA level and protein expression.

Claim 13 (Canceled).

14. (Previously presented) The method according to claim 1, characterised in that the selection is performed in such a way as to give a first knowledge base comprising only one set of selected genes.

15. (Previously presented) The method according to claim 1, characterised in that the selection is performed in such a way as to give a first knowledge base comprising different subsets of selected genes.

16. (Previously presented) The method according to claim 1, characterised in that the selection is at least partially performed automatically by means of at least one of a robot and a computer device.

17. (Previously presented) The method according to claim 1, characterised in that at

least two genes are selected in parallel.

18. (Previously presented) The method according to claim 17, characterised in that at least 100 genes are selected in parallel.

Claim 19 (Canceled).

20. (Previously presented) The method according to claim 1, characterised in that the analysis of the level of cytosine methylation comprises polymerase chain reaction (PCR), hybridisation analyses, sequencing, mass spectrometry and fluorescent, enzymatic, radioactive, dye and/or antibody labelling.

21. (Previously presented) The method according to claim 1, characterised in that the analysis of the level of cytosine methylation is at least partially performed by means of at least one of a robot and a computer device.

22. (Previously presented) The method according to claim 1, characterised in that the level of cytosine methylation of at least two genes are analysed in parallel.

23. (Previously presented) The method according claim 22, characterised in that the level of cytosine methylation of at least 100 genes are analysed in parallel.

Claim 24 (Canceled).

25. (Previously presented) The method according to claim 1, characterised in that the selection is performed in such a way as to give a second knowledge base comprising only one set of selected genes.

26. (Previously presented) The method according to claim 1, characterised in that the selection is performed in such a way as to give a second knowledge base comprising different subsets of selected genes.

Claims 27-29 (Canceled).

30. (Previously presented) The method according to claim 1, characterised in that all or a part of the genes of the second knowledge base are added to the gene panel.

31. (Previously presented) The method according to claim 1, characterised in that additional information about the selected genes is added to the gene panel.

32. (Previously presented) The method according to claim 1, characterised in that steps a) to f) are repeated.

33. (Previously presented) The method according to claim 32, characterised in that it is repeated for at least 100 times.

34. (Previously presented) The method according to claim 32, characterised in that identical biological material, different biological material or a combination thereof is used in step a).

Claim 35 (Canceled).

36. (Previously presented) The method according to claim 1, characterised in that it is at least partially performed by means of at least one of a robot and a computer device.

Claims 37-40 (Canceled).

41. (Previously presented) A device for the generation of a gene panel for diagnostic and therapeutic purposes, comprising means for generating a first and second knowledge base according to claim 1; and means for adding selected genes from the second knowledge base to a gene panel.

Claims 42-58 (Canceled).